

SEQUENCE LISTING

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<120> MODIFIED PLASMINOGEN ACTIVATOR INHIBITOR
TYPE-1 AND METHODS BASED THEREON

<130> 9471-011-999

<140> to be assigned (National Stage of PCT/US03/06679)
<141> 2003-03-04 (PCT filing date)

<150> PCT/US03/06679
<151> 2003-03-04

<150> 60/361,670
<151> 2002-03-04

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 2876
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (76)...(1281)
<223> human PAI-1 plus 5' and 3' sequence

<400> 1
gaattcctgc agctcagcag ccggccgccag agcaggacga accgccaatc gcaaggcacc 60
tctgagaact tcagg atg cag atg tct cca gcc ctc acc tgc cta gtc ctg 111
Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu
1 5 10

ggc ctg gcc ctt gtc ttt ggt gaa ggg tct gct gtg cac cat ccc cca 159
Gly Leu Ala Leu Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro
15 20 25

tcc tac gtg gcc cac ctg gcc tca gac ttc ggg gtg agg gtg ttt cag 207
Ser Tyr Val Ala His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln
30 35 40

cag gtg gcg cag gcc tcc aag gac cgc aac gtg gtt ttc tca ccc tat 255
Gln Val Ala Gln Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr
45 50 55 60

ggg gtg gcc tcg gtg ttg gcc atg ctc cag ctg aca aca gga gga gaa 303
Gly Val Ala Ser Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu
65 70 75

acc cag cag cag att caa gca gct atg gga ttc aag att gat gac aag 351
Thr Gln Gln Gln Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys

80	85	90	
ggc atg gcc ccc gcc ctc cg	cat ctg tac aag gag ctc atg ggg cca		399
Gly Met Ala Pro Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro			
95	100	105	
tgg aac aag gat gag atc agc acc aca gac gcg atc ttc gtc cag cg			447
Trp Asn Lys Asp Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg			
110	115	120	
gat ctg aag ctg gtc cag ggc ttc atg ccc cac ttc ttc agg ctg ttc			495
Asp Leu Lys Leu Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe			
125	130	135	140
cgg agc acg gtc aag caa gtg gac ttt tca gag gtg gag aga gcc aga			543
Arg Ser Thr Val Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg			
145	150	155	
ttc atc atc aat gac tgg gtg aag aca cac aca aaa ggt atg atc agc			591
Phe Ile Ile Asn Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser			
160	165	170	
aac ttg ctt ggg aaa gga gcc gtg gac cag ctg aca cgg ctg gtg ctg			639
Asn Leu Leu Gly Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu			
175	180	185	
gtg aat gcc ctc tac ttc aac ggc cag tgg aag act ccc ttc ccc gac			687
Val Asn Ala Leu Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp			
190	195	200	
tcc agc acc cac cgc cgc ctc ttc cac aaa tca gac ggc agc act gtc			735
Ser Ser Thr His Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val			
205	210	215	220
tct gtg ccc atg atg gct cag acc aac aag ttc aac tat act gag ttc			783
Ser Val Pro Met Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe			
225	230	235	
acc acg ccc gat ggc cat tac tac gac atc ctg gaa ctg ccc tac cac			831
Thr Thr Pro Asp Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His			
240	245	250	
ggg gac acc ctc agc atg ttc att gct gcc cct tat gaa aaa gag gtg			879
Gly Asp Thr Leu Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val			
255	260	265	
cct ctc tct gcc ctc acc aac att ctg agt gcc cag ctc atc agc cac			927
Pro Leu Ser Ala Leu Thr Asn Ile Leu Ser Ala Gln Leu Ile Ser His			
270	275	280	
tgg aaa ggc aac atg acc agg ctg ccc cgc ctc ctg gtt ctg ccc aag			975
Trp Lys Gly Asn Met Thr Arg Leu Pro Arg Leu Leu Val Leu Pro Lys			
285	290	295	300
ttc tcc ctg gag act gaa gtc gac ctc agg aag ccc cta gag aac ctg			1023
Phe Ser Leu Glu Thr Glu Val Asp Leu Arg Lys Pro Leu Glu Asn Leu			
305	310	315	
gga atg acc gac atg ttc aga cag ttt cag gct gac ttc acg agt ctt			1071
Gly Met Thr Asp Met Phe Arg Gln Phe Gln Ala Asp Phe Thr Ser Leu			
320	325	330	

<210> 2
<211> 402
<212> PRT
<213> Home sapiens

<220>
<223> human PAI-1 amino acid sequence, including signal peptide

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Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu Gly Leu Ala Leu
1 5 10 15
Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro Ser Tyr Val Ala

20	25	30	
His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln Gln Val Ala Gln			
35	40	45	
Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr Gly Val Ala Ser			
50	55	60	
Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu Thr Gln Gln Gln			
65	70	75	80
Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys Gly Met Ala Pro			
85	90	95	
Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro Trp Asn Lys Asp			
100	105	110	
Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg Asp Leu Lys Leu			
115	120	125	
Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe Arg Ser Thr Val			
130	135	140	
Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg Phe Ile Ile Asn			
145	150	155	160
Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser Asn Leu Leu Gly			
165	170	175	
Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu Val Asn Ala Leu			
180	185	190	
Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp Ser Ser Thr His			
195	200	205	
Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val Ser Val Pro Met			
210	215	220	
Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe Thr Thr Pro Asp			
225	230	235	240
Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His Gly Asp Thr Leu			
245	250	255	
Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val Pro Leu Ser Ala			
260	265	270	
Leu Thr Asn Ile Leu Ser Ala Gln Leu Ile Ser His Trp Lys Gly Asn			
275	280	285	
Met Thr Arg Leu Pro Arg Leu Leu Val Leu Pro Lys Phe Ser Leu Glu			
290	295	300	
Thr Glu Val Asp Leu Arg Lys Pro Leu Glu Asn Leu Gly Met Thr Asp			
305	310	315	320
Met Phe Arg Gln Phe Gln Ala Asp Phe Thr Ser Leu Ser Asp Gln Glu			
325	330	335	
Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys Ile Glu Val Asn			
340	345	350	
Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val Ile Val Ser Ala			
355	360	365	
Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro Phe Leu Phe Val			
370	375	380	
Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met Gly Gln Val Met			
385	390	395	400
Glu Pro			

<210> 3
 <211> 379
 <212> PRT
 <213> Home sapiens

<220>
 <223> human PAI-1 mature amino acid sequence

<400> 3
 Val His His Pro Pro Ser Tyr Val Ala His Leu Ala Ser Asp Phe Gly
 1 5 10 15

Val Arg Val Phe Gln Gln Val Ala Gln Ala Ser Lys Asp Arg Asn Val
20 25 30
Val Phe Ser Pro Tyr Gly Val Ala Ser Val Leu Ala Met Leu Gln Leu
35 40 45
Thr Thr Gly Gly Glu Thr Gln Gln Ile Gln Ala Ala Met Gly Phe
50 55 60
Lys Ile Asp Asp Lys Gly Met Ala Pro Ala Leu Arg His Leu Tyr Lys
65 70 75 80
Glu Leu Met Gly Pro Trp Asn Lys Asp Glu Ile Ser Thr Thr Asp Ala
85 90 95
Ile Phe Val Gln Arg Asp Leu Lys Leu Val Gln Gly Phe Met Pro His
100 105 110
Phe Phe Arg Leu Phe Arg Ser Thr Val Lys Gln Val Asp Phe Ser Glu
115 120 125
Val Glu Arg Ala Arg Phe Ile Ile Asn Asp Trp Val Lys Thr His Thr
130 135 140
Lys Gly Met Ile Ser Asn Leu Leu Gly Lys Gly Ala Val Asp Gln Leu
145 150 155 160
Thr Arg Leu Val Leu Val Asn Ala Leu Tyr Phe Asn Gly Gln Trp Lys
165 170 175
Thr Pro Phe Pro Asp Ser Ser Thr His Arg Arg Leu Phe His Lys Ser
180 185 190
Asp Gly Ser Thr Val Ser Val Pro Met Met Ala Gln Thr Asn Lys Phe
195 200 205
Asn Tyr Thr Glu Phe Thr Thr Pro Asp Gly His Tyr Tyr Asp Ile Leu
210 215 220
Glu Leu Pro Tyr His Gly Asp Thr Leu Ser Met Phe Ile Ala Ala Pro
225 230 235 240
Tyr Glu Lys Glu Val Pro Leu Ser Ala Leu Thr Asn Ile Leu Ser Ala
245 250 255
Gln Leu Ile Ser His Trp Lys Gly Asn Met Thr Arg Leu Pro Arg Leu
260 265 270
Leu Val Leu Pro Lys Phe Ser Leu Glu Thr Glu Val Asp Leu Arg Lys
275 280 285
Pro Leu Glu Asn Leu Gly Met Thr Asp Met Phe Arg Gln Phe Gln Ala
290 295 300
Asp Phe Thr Ser Leu Ser Asp Gln Glu Pro Leu His Val Ala Gln Ala
305 310 315 320
Leu Gln Lys Val Lys Ile Glu Val Asn Glu Ser Gly Thr Val Ala Ser
325 330 335
Ser Ser Thr Ala Val Ile Val Ser Ala Arg Met Ala Pro Glu Glu Ile
340 345 350
Ile Met Asp Arg Pro Phe Leu Phe Val Val Arg His Asn Pro Thr Gly
355 360 365
Thr Val Leu Phe Met Gly Gln Val Met Glu Pro
370 375